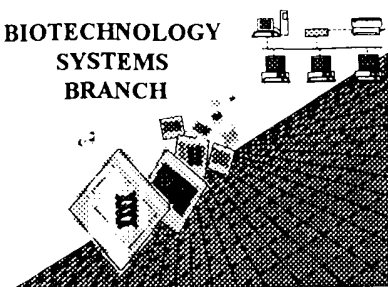


0590  
12/11/01

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/893,666  
Source: OIP/E  
Date Processed by STIC: 12/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/893,666
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ✓ _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/893,666

DATE: 12/06/2001

TIME: 10:36:14

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

3 <110> APPLICANT: YAMASHITA, ICHIRO  
 5 <120> TITLE OF INVENTION: High estrogen-sensitive medaka fish  
 7 <130> FILE REFERENCE: 210217US-620-7249-0  
 9 <140> CURRENT APPLICATION NUMBER: US 09/893,666  
 10 <141> CURRENT FILING DATE: 2001-06-29  
 12 <150> PRIOR APPLICATION NUMBER: JP 2000-247729  
 13 <151> PRIOR FILING DATE: 2000-08-17  
 15 <160> NUMBER OF SEQ ID NOS: 7  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2764  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Oryzias latipes  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (211)..(1935)  
 27 <223> OTHER INFORMATION:  
 30 <400> SEQUENCE: 1

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33	atctgaggat gattcatgag taagagacag agctcgggtgc agatcaggca gctgttcgga	120
35	ccagcaactca gatccaggat cagcccgagcc tctcagagc tggagaccct ctccccacct	180
37	cgccctctcgc cccgtgaccc cctcgggtgac atg tac cct gaa gag agc cgg ggt	234
38	Met Tyr Pro Glu Glu Ser Arg Gly	
39	1 5	
41	tct gga ggg gtg gct gct gtg gac ttt ttg gaa ggg acg tac gac tat	282
42	Ser Gly Gly Val Ala Ala Val Asp Phe Leu Glu Gly Thr Tyr Asp Tyr	
43	10 15 20	
45	gcc gcc ccc aac cct gcc acg act ccc ctt tac agc cag tcc agc acc	330
46	Ala Ala Pro Asn Pro Ala Thr Thr Pro Leu Tyr Ser Gln Ser Ser Thr	
47	25 30 35 40	
49	ggc tac tac tct gct ccc ctg gaa aca aac gga ccc ccc tca gaa ggc	378
50	Gly Tyr Tyr Ser Ala Pro Leu Glu Thr Asn Gly Pro Pro Ser Glu Gly	
51	45 50 55	
53	agt ctg cag tcc ctg ggc agt ggg ccg acg agc cct ctg gtg ttt gtg	426
54	Ser Leu Gln Ser Leu Gly Ser Gly Pro Thr Ser Pro Leu Val Phe Val	
55	60 65 70	
57	ccc tcc agc ccc aga ctc agt ccc ttt atg cat cca ccc agc cac cac	474
58	Pro Ser Ser Pro Arg Leu Ser Pro Phe Met His Pro Pro Ser His His	
59	75 80 85	
61	tat ctg gaa acc act tcc acg ccc gtt tac aga tcc agc cac cag gga	522
62	Tyr Leu Glu Thr Thr Ser Thr Pro Val Tyr Arg Ser Ser His Gln Gly	
63	90 95 100	
65	gcc tcc agg gag gac cag tgc ggc tcc cgg gag gac acg tgc agc ctg	570
66	Ala Ser Arg Glu Asp Gln Cys Gly Ser Arg Glu Asp Thr Cys Ser Leu	
67	105 110 115 120	
69	ggg gag tta ggc gcc gga gcc ggg gct ggg ggg ttt gag atg gcc aaa	618
70	Gly Glu Leu Gly Ala Gly Ala Gly Ala Gly Gly Phe Glu Met Ala Lys	

Does Not Comply  
Corrected Sequence

P.6

## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/893,666

TIME: 10:36:14

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

71		125		130		135	
73	gac acg cgt ttc tgc gcc gtg tgc agc gac tac gcc tct ggg tac cac					666	
74	Asp Thr Arg Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His						
75		140		145		150	
77	tat ggg gtg tgg tct tgt gag ggc tgc aag gcc ttc ttc aag agg agc					714	
78	Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser						
79		155		160		165	
81	atc cag ggt cac aat gac tat atg tgc cca gcg acc aat cag tgc act					762	
82	Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr						
83		170		175		180	
85	att gac aga aat cgg agg aag agc tgc cag gct tgt cgt ctt agg aag					810	
86	Ile Asp Arg Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys						
87	185		190		195	200	
89	tgt tac gaa gtg gga atg atg aaa ggc ggt gtg cgc aag gac cgc att					858	
90	Cys Tyr Glu Val Gly Met Met Lys Gly Gly Val Arg Lys Asp Arg Ile						
91		205		210		215	
93	cgc att tta cgg cgt gac aaa cgg cgg aca ggc gtt ggt gat gga gac					906	
94	Arg Ile Leu Arg Arg Asp Lys Arg Arg Thr Gly Val Gly Asp Gly Asp						
95		220		225		230	
97	aag gtt gta aag ggt cag gag cat aaa acg gtg cat tat gat gga agg					954	
98	Lys Val Val Lys Gly Gln Glu His Lys Thr Val His Tyr Asp Gly Arg						
99		235		240		245	
101	aaa cgc agc agc aca gga gga gga gga gga gga gga gga aga ctg					1002	
102	Lys Arg Ser Ser Thr Gly Gly Gly Gly Gly Gly Gly Gly Arg Leu						
103		250		255		260	
105	tct gtg acc agc ata cct cct gag cag gtg ctg ctc ctc ctt cag ggc					1050	
106	Ser Val Thr Ser Ile Pro Pro Glu Gln Val Leu Leu Leu Gln Gly						
107	265		270		275	280	
109	gcc gag ccc ccg ata ctc tgc tgc cgt cag aag ttg agc cga ccg tac					1098	
110	Ala Glu Pro Pro Ile Leu Cys Ser Arg Gln Lys Leu Ser Arg Pro Tyr						
111		285		290		295	
113	acc gag gtc acc atg atg acc ctg ctc acc agc atg gca gac aag gag					1146	
114	Thr Glu Val Thr Met Met Thr Leu Leu Thr Ser Met Ala Asp Lys Glu						
115		300		305		310	
117	ctg gtc cac atg atc gcc tgg gcc aag aag ctc cca ggt ttt ctg cag					1194	
118	Leu Val His Met Ile Ala Trp Ala Lys Lys Leu Pro Gly Phe Leu Gln						
119		315		320		325	
121	ctg tcc ctg cac gat cag gtg ctg ctg ctg gag agc tgc tgg ctg gag					1242	
122	Leu Ser Leu His Asp Gln Val Leu Leu Leu Glu Ser Ser Trp Leu Glu						
123		330		335		340	
125	gtg ctc atg atc ggc ctc att tgg agg tcc atc cac tgt ccc ggg aag					1290	
126	Val Leu Met Ile Gly Leu Ile Trp Arg Ser Ile His Cys Pro Gly Lys						
127	345		350		355	360	
129	ctc atc ttt gca caa gac ctc atc ctg gac agg aat gag gga gac tgc					1338	
130	Leu Ile Phe Ala Gln Asp Leu Ile Leu Asp Arg Asn Glu Gly Asp Cys						
131		365		370		375	
133	gtg gaa ggc atg acg gag atc ttc gac atg ctg ctg gcc act gct tcc					1386	
134	Val Glu Gly Met Thr Glu Ile Phe Asp Met Leu Leu Ala Thr Ala Ser						
135		380		385		390	

## RAW SEQUENCE LISTING

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TIME: 10:36:14

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

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137 cgc ttc cgt gtg ctc aaa ctc aaa cct gag gaa ttc gtc tgc ctc aaa      1434
138 Arg Phe Arg Val Leu Lys Leu Lys Pro Glu Glu Phe Val Cys Leu Lys
139          395          400          405
141 gct att att tta ctc aac tcc ggt gct ttt tct ttc tgc acc ggc acc      1482
142 Ala Ile Ile Leu Leu Asn Ser Gly Ala Phe Ser Phe Cys Thr Gly Thr
143      410          415          420
145 atg gag cca ctt cac aac agc gcg gcg gtt cag agc atg ctg gac acc      1530
146 Met Glu Pro Leu His Asn Ser Ala Ala Val Gln Ser Met Leu Asp Thr
147 425          430          435          440
149 atc aca gac gca ctc att cat tac atc agt cag tcg ggt tac ttg gcc      1578
150 Ile Thr Asp Ala Leu Ile His Tyr Ile Ser Gln Ser Gly Tyr Leu Ala
151          445          450          455
153 cag gag cag gcg aga cgg cag gcc cag ctg ctc ctg ctg ctc tcc cac      1626
154 Gln Glu Gln Ala Arg Arg Gln Ala Gln Leu Leu Leu Leu Leu Ser His
155      460          465          470
157 atc agg cac atg agc aac aaa ggc atg gag cac ctc tac agc atg aag      1674
158 Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met Lys
159      475          480          485
161 tgc aag aac aaa gtc cct ctt tat gac ctc cta ctg gag atg ctc gat      1722
162 Cys Lys Asn Lys Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu Asp
163      490          495          500
165 gcc cac cgc ctg cac cac ccc gtc aga gca ccc cag tcc ttg tcc caa      1770
166 Ala His Arg Leu His His Pro Val Arg Ala Pro Gln Ser Leu Ser Gln
167 505          510          515          520
169 gtc gac aga gac cct ccc tcc acc agc agc ggc ggg ggt gga atc gct      1818
170 Val Asp Arg Asp Pro Ser Thr Ser Ser Gly Gly Gly Gly Ile Ala
171          525          530          535
173 ccc ggt tct ata tca gca tct cga ggc aga atc gag agt ccg agc aga      1866
174 Pro Gly Ser Ile Ser Ala Ser Arg Gly Arg Ile Glu Ser Pro Ser Arg
175      540          545          550
177 ggc ccc ttt gct ccc agt gtc ctt cag tat gga ggg tcg cgt cct gac      1914
178 Gly Pro Phe Ala Pro Ser Val Leu Gln Tyr Gly Gly Ser Arg Pro Asp
179      555          560          565
181 tgc acc ccg gcc ctt caa gac tgagcacaca gtccaaggcc ctttttttgt      1965
182 Cys Thr Pro Ala Leu Gln Asp
183      570          575
185 ggctcaaggg ttcagggttg gacaaggtga tgcttgattt aattttaaga attatttata      2025
187 aataagagtg gcgctgagag gagaagctcc cacaatgaac tgccctctgct tggctccagct      2085
189 tttgtgcagt cactttaatc tgcttatatt catctccttt gtaaaccctga gcgtctcttt      2145
191 agcagctttt ttttgccttc caaacagcat gtggtagatt gtaagggttc gtcccatgag      2205
193 ttctggtgat ttcaagaaaa tgagcagcta atgttttctg taaccgtctt gacccaagtg      2265
195 cacttccctct tggattaaag gggctaattg gcattatttt gtctcttgta catatgggat      2325
197 ggctaagaat aatgagagta attgtcagat tttgtgtaga acttaccac aaatgcaatt      2385
199 ttaaaataag atttaaaaac aaaagaggca agatcaaacc tgagagcaact gaagacacgc      2445
201 tgtagaaagc tgggtaaat tgttatccac gtctatctct ggaaaggact ttgttctctg      2505
203 tgcctgcagc tcatttactc tgaacttgct acttggtgaa catttggtgca cttgtccgtg      2565
205 tttttctagc actgtagctt atgaacgctg agaaagaatc taatgctttg atgcacagat      2625
207 ttgccttgta ttgtacatct cagccacaaa cgtacttttc gtccacaagt tgactgactg      2685
209 caccttgatt aaattgtcta aaagttcatt taaatgttga attctgtgaa aattaaaaag      2745

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## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/893,666

TIME: 10:36:14

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

2764

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211 gcaattcctg ttctattt
214 <210> SEQ ID NO: 2
215 <211> LENGTH: 575
216 <212> TYPE: PRT
217 <213> ORGANISM: Oryzias latipes
219 <400> SEQUENCE: 2
221 Met Tyr Pro Glu Glu Ser Arg Gly Ser Gly Gly Val Ala Ala Val Asp
222 1 5 10 15
225 Phe Leu Glu Gly Thr Tyr Asp Tyr Ala Ala Pro Asn Pro Ala Thr Thr
226 20 25 30
229 Pro Leu Tyr Ser Gln Ser Ser Thr Gly Tyr Tyr Ser Ala Pro Leu Glu
230 35 40 45
233 Thr Asn Gly Pro Pro Ser Glu Gly Ser Leu Gln Ser Leu Gly Ser Gly
234 50 55 60
237 Pro Thr Ser Pro Leu Val Phe Val Pro Ser Ser Pro Arg Leu Ser Pro
238 65 70 75 80
241 Phe Met His Pro Pro Ser His His Tyr Leu Glu Thr Thr Ser Thr Pro
242 85 90 95
245 Val Tyr Arg Ser Ser His Gln Gly Ala Ser Arg Glu Asp Gln Cys Gly
246 100 105 110
249 Ser Arg Glu Asp Thr Cys Ser Leu Gly Glu Leu Gly Ala Gly Ala Gly
250 115 120 125
253 Ala Gly Gly Phe Glu Met Ala Lys Asp Thr Arg Phe Cys Ala Val Cys
254 130 135 140
257 Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly
258 145 150 155 160
261 Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met
262 165 170 175
265 Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Arg Asn Arg Arg Lys Ser
266 180 185 190
269 Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys
270 195 200 205
273 Gly Gly Val Arg Lys Asp Arg Ile Arg Ile Leu Arg Arg Asp Lys Arg
274 210 215 220
277 Arg Thr Gly Val Gly Asp Gly Asp Lys Val Val Lys Gly Gln Glu His
278 225 230 235 240
281 Lys Thr Val His Tyr Asp Gly Arg Lys Arg Ser Ser Thr Gly Gly Gly
282 245 250 255
285 Gly Gly Gly Gly Gly Gly Arg Leu Ser Val Thr Ser Ile Pro Pro Glu
286 260 265 270
289 Gln Val Leu Leu Leu Leu Gln Gly Ala Glu Pro Pro Ile Leu Cys Ser
290 275 280 285
293 Arg Gln Lys Leu Ser Arg Pro Tyr Thr Glu Val Thr Met Met Thr Leu
294 290 295 300
297 Leu Thr Ser Met Ala Asp Lys Glu Leu Val His Met Ile Ala Trp Ala
298 305 310 315 320
301 Lys Lys Leu Pro Gly Phe Leu Gln Leu Ser Leu His Asp Gln Val Leu
302 325 330 335
305 Leu Leu Glu Ser Ser Trp Leu Glu Val Leu Met Ile Gly Leu Ile Trp

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/893,666

DATE: 12/06/2001

TIME: 10:36:14

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

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306          340          345          350
309 Arg Ser Ile His Cys Pro Gly Lys Leu Ile Phe Ala Gln Asp Leu Ile
310          355          360          365
313 Leu Asp Arg Asn Glu Gly Asp Cys Val Glu Gly Met Thr Glu Ile Phe
314          370          375          380
317 Asp Met Leu Leu Ala Thr Ala Ser Arg Phe Arg Val Leu Lys Leu Lys
318 385          390          395          400
321 Pro Glu Glu Phe Val Cys Leu Lys Ala Ile Ile Leu Leu Asn Ser Gly
322          405          410          415
325 Ala Phe Ser Phe Cys Thr Gly Thr Met Glu Pro Leu His Asn Ser Ala
326          420          425          430
329 Ala Val Gln Ser Met Leu Asp Thr Ile Thr Asp Ala Leu Ile His Tyr
330          435          440          445
333 Ile Ser Gln Ser Gly Tyr Leu Ala Gln Glu Gln Ala Arg Arg Gln Ala
334          450          455          460
337 Gln Leu Leu Leu Leu Leu Ser His Ile Arg His Met Ser Asn Lys Gly
338 465          470          475          480
341 Met Glu His Leu Tyr Ser Met Lys Cys Lys Asn Lys Val Pro Leu Tyr
342          485          490          495
345 Asp Leu Leu Leu Glu Met Leu Asp Ala His Arg Leu His His Pro Val
346          500          505          510
349 Arg Ala Pro Gln Ser Leu Ser Gln Val Asp Arg Asp Pro Pro Ser Thr
350          515          520          525
353 Ser Ser Gly Gly Gly Gly Ile Ala Pro Gly Ser Ile Ser Ala Ser Arg
354          530          535          540
357 Gly Arg Ile Glu Ser Pro Ser Arg Gly Pro Phe Ala Pro Ser Val Leu
358 545          550          555          560
361 Gln Tyr Gly Gly Ser Arg Pro Asp Cys Thr Pro Ala Leu Gln Asp
362          565          570          575

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365 &lt;210&gt; SEQ ID NO: 3

366 &lt;211&gt; LENGTH: 20

367 &lt;212&gt; TYPE: DNA

368 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

370 &lt;220&gt; FEATURE:

371 &lt;223&gt; OTHER INFORMATION: SYNTHETIC DNA

373 &lt;400&gt; SEQUENCE: 3

374 tgggtgacat gtaccctgaa

20

377 &lt;210&gt; SEQ ID NO: 4

378 &lt;211&gt; LENGTH: 20

379 &lt;212&gt; TYPE: DNA

380 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

382 &lt;220&gt; FEATURE:

383 &lt;223&gt; OTHER INFORMATION: SYNTHETIC DNA

385 &lt;400&gt; SEQUENCE: 4

386 ctgtgtgctc agtcttgaag

20

389 &lt;210&gt; SEQ ID NO: 5

390 &lt;211&gt; LENGTH: 20

391 &lt;212&gt; TYPE: DNA

392 &lt;213&gt; ORGANISM: ARTIFICIAL SEQUENCE

<210> 6  
<211> 20  
<212> DNA  
<213> ARTIFICIAL DNA

see item 10 on Error Summary sheet

<400> 6  
gtaggagggtc ataaagaggg



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/893,666

DATE: 12/06/2001

TIME: 10:36:15

Input Set : A:\210217US0.ST25.txt

Output Set: N:\CRF3\12062001\I893666.raw

L:404 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6

L:406 M:258 W: Mandatory Feature missing, <220> FEATURE:

L:406 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: